



A service of the National Library of Medicine
and the National Institutes of Health

[My NCBI](#) [?](#)
[\[Sign In\]](#) [\[Register\]](#)

All Databases

PubMed

Nucleotide

Protein

Genome

Structure

OMIM

PMC

Journals

Books

Search **PubMed**

for

[Preview](#)[Go](#)[Clear](#)

Limits Preview/Index **History** Clipboard Details

- Search History will be lost after eight hours of inactivity.
- Search numbers may not be continuous; all searches are represented.
- To save search indefinitely, click query # and select Save in My NCBI.
- To combine searches use #search, e.g., #2 AND #3 or click query # for more options.

About Entrez

Text Version

Entrez PubMed

Overview

Help | FAQ

Tutorials

New/Noteworthy

E-Utilities

PubMed Services

Journals Database

MeSH Database

Single Citation Matcher

Batch Citation Matcher

Clinical Queries

Special Queries

LinkOut

My NCBI

Related Resources

Order Documents

NLM Mobile

NLM Catalog

NLM Gateway

TOXNET

Consumer Health

Clinical Alerts

ClinicalTrials.gov

PubMed Central

Search	Most Recent Queries	Time	Result
#65	Search ("Oxytocics"[MeSH] OR "Abortifacient Agents"[MeSH]) AND (calgranulin* OR "s-100" OR "s100" OR "s 100" OR "s100a8" OR "s100-a8" OR "60b8 b" OR "60b8-b" OR "60b8b" OR "cabp-p8" OR "cabp p8" OR "cabpp8" OR "cystic fibrosis antigen" OR "leukocyte II protein" OR "macrophage related protein 8" OR "macrophage related protein-8" OR "mrp-8" OR "mrp8" OR "mrp 8" OR "myeloid calcium" OR "s100a12" OR "s100-a12" OR cgrp OR "caaf1" OR enrage OR "en-rage" OR p6 OR "calgranulin related protein" OR calcitermin)	21:31:19	0
#50	Search "S100 Proteins"[MAJR] AND (calgranulin* OR "s-100" OR "s100" OR "s 100" OR "s100a8" OR "s100-a8" OR "60b8 b" OR "60b8-b" OR "60b8b" OR "cabp-p8" OR "cabp p8" OR "cabpp8" OR "cystic fibrosis antigen" OR "leukocyte II protein" OR "macrophage related protein 8" OR "macrophage related protein-8" OR "mrp-8" OR "mrp8" OR "mrp 8" OR "myeloid calcium" OR "s100a12" OR "s100-a12" OR cgrp OR "caaf1" OR enrage OR "en-rage" OR p6 OR "calgranulin related protein" OR calcitermin) AND (fetus OR fetal)	20:28:33	94
#49	Search "S100 Proteins"[MAJR] AND (calgranulin* OR "s-100" OR "s100" OR "s 100" OR "s100a8" OR "s100-a8" OR "60b8 b" OR "60b8-b" OR "60b8b" OR "cabp-p8" OR "cabp p8" OR "cabpp8" OR "cystic fibrosis antigen" OR "leukocyte II protein" OR "macrophage related protein 8" OR "macrophage related protein-8" OR "mrp-8" OR "mrp8" OR "mrp 8" OR "myeloid calcium" OR "s100a12" OR "s100-a12" OR cgrp OR "caaf1" OR enrage OR "en-rage" OR p6 OR "calgranulin related protein" OR calcitermin)	20:27:47	2978
#48	Search "S100 Proteins"[MeSH] AND (calgranulin* OR "s-100" OR "s100" OR "s 100" OR "s100a8" OR "s100-a8" OR "60b8 b" OR "60b8-b" OR "60b8b" OR "cabp-p8" OR "cabp p8" OR "cabpp8" OR "cystic fibrosis antigen" OR "leukocyte II protein" OR "macrophage related protein 8" OR "macrophage related protein-8" OR "mrp-8" OR "mrp8" OR "mrp 8" OR "myeloid calcium" OR "s100a12" OR "s100-a12" OR cgrp OR "caaf1" OR enrage OR "en-rage" OR p6 OR "calgranulin related protein" OR calcitermin)	20:27:24	7204
#45	Search (calgranulin* OR "s-100" OR "s100" OR "s 100" OR "s100a8" OR "s100-a8" OR "60b8 b" OR "60b8-b" OR "60b8b" OR "cabp-p8" OR "cabp p8" OR "cabpp8" OR "cystic fibrosis antigen" OR "leukocyte II protein" OR "macrophage related protein 8" OR "macrophage related protein-8" OR "mrp-8" OR "mrp8" OR "mrp 8" OR "myeloid calcium" OR "s100a12" OR "s100-a12" OR cgrp OR "caaf1" OR enrage OR "en-rage" OR p6 OR "calgranulin related protein" OR calcitermin) AND amnio*	20:05:48	52
#44	Search (calgranulin* OR "s-100" OR "s100" OR "s 100" OR "s100a8" OR "s100-a8" OR "60b8 b" OR "60b8-b" OR "60b8b" OR "cabp-p8" OR "cabp p8" OR "cabpp8" OR "cystic fibrosis antigen" OR "leukocyte II protein" OR "macrophage related protein 8" OR "macrophage related protein-8" OR "mrp-8" OR "mrp8" OR "mrp 8" OR "myeloid calcium") AND ("s100a12" OR "s100-a12" OR cgrp OR "caaf1" OR enrage OR "en-rage" OR p6 OR "calgranulin related protein" OR calcitermin) AND amnio*	20:04:29	6
#42	Search (calgranulin* OR "s-100" OR "s100" OR "s 100") AND ("s100a8" OR "s100-a8" OR "60b8 b" OR "60b8-b" OR "60b8b" OR "cabp-p8" OR "cabp p8" OR "cabpp8" OR "cystic fibrosis antigen" OR "leukocyte II protein" OR "macrophage related protein 8" OR "macrophage related protein-8" OR	20:02:33	2

"mrp-8" OR "mrp8" OR "mrp 8" OR "myeloid calcium") and ("s100a12" OR "s100-a12" OR cgrp OR "caaf1" OR enrage OR "en-rage" OR p6 OR "calgranulin related protein" OR calcitermin) AND amnio*		
#37 Related Articles for PubMed (Select 8718672) sort by: PublicationDate	19:49:00	171
#33 Search (calgranulin* OR "s-100" OR "s100" OR "s 100") and ("s100a8" OR "s100-a8" OR "60b8 b" OR "60b8-b" OR "60b8b" OR "cabp-p8" OR "cabp p8" OR "cabpp8" OR "cystic fibrosis antigen" OR "leukocyte II protein" OR "macrophage related protein 8" OR "macrophage related protein-8" OR "mrp-8" OR "mrp8" OR "mrp 8" OR "myeloid calcium") and ("s100a12" OR "s100-a12" OR cgrp OR "caaf1" OR enrage OR "en-rage" OR p6 OR "calgranulin related protein" OR calcitermin)	19:44:01	131
#32 Search (calgranulin\$ OR "s-100" OR "s100" OR "s 100") and ("s100a8" OR "s100-a8" OR "60b8 b" OR "60b8-b" OR "60b8b" OR "cabp-p8" OR "cabp p8" OR "cabpp8" OR "cystic fibrosis antigen" OR "leukocyte II protein" OR "macrophage related protein 8" OR "macrophage related protein-8" OR "mrp-8" OR "mrp8" OR "mrp 8" OR "myeloid calcium") and ("s100a12" OR "s100-a12" OR cgrp OR "caaf1" OR enrage OR "en-rage" OR p6 OR "calgranulin related protein" OR calcitermin)	19:42:48	134
#30 Search ("Calcitonin Gene-Related Peptide"[MeSH] OR "Receptors, Calcitonin Gene-Related Peptide"[MeSH]) AND ("Amniotic Fluid"[MeSH] OR "Amniocentesis"[MeSH])	19:17:27	2
#24 Search "S100 Proteins"[MeSH] AND ("Amniotic Fluid"[MeSH] OR "Amniocentesis"[MeSH])	18:57:33	27
#19 Search "S100 Proteins"[MAJR] AND ("Amniotic Fluid"[MeSH] OR "Amniocentesis"[MeSH])	18:54:39	20
#15 Search "S100 Proteins"[MAJR]	18:53:39	3062
#14 Search "S100 Proteins"[MeSH]	18:53:27	7778

[Clear History](#)[Write to the Help Desk](#)[NCBI](#) | [NLM](#) | [NIH](#)[Department of Health & Human Services](#)[Privacy Statement](#) | [Freedom of Information Act](#) | [Disclaimer](#).

Apr 4 2007 12:47:27

UniProtKB/Swiss-Prot entry P05109

Entry information

Entry name	S10A8_HUMAN
Primary accession number	P05109
Secondary accession numbers	Q5SY70 Q9UC92 Q9UCJ0
Integrated into Swiss-Prot on	August 13, 1987
Sequence was last modified on	January 1, 1988 (Sequence version 1)
Annotations were last modified on	March 20, 2007 (Entry version 87)

Name and origin of the protein

Protein name	Protein S100-A8
Synonyms	S100 calcium-binding protein A8 Calgranulin-A Migration inhibitory factor-related protein 8 MRP-8 Cystic fibrosis antigen CFAG P8 Leukocyte L1 complex light chain Calprotectin L1L subunit Urinary stone protein band A
Gene name	Name: S100A8
From	Synonyms: CAGA, MRP8
Taxonomy	Homo sapiens (Human) [TaxID: 9606] Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

References

- [1] NUCLEOTIDE SEQUENCE [mRNA].
DOI=10.1038/326614a0; PubMed=3561500
Dorin J.R., Novak M., Hill R.E., Brock D.J.H., Secher D.S., van Heyningen V.;
"A clue to the basic defect in cystic fibrosis from cloning the CF antigen gene."; Nature 326:614-617(1987).
- [2] NUCLEOTIDE SEQUENCE [mRNA].
DOI=10.1038/330080a0; PubMed=3313057
Ondink K., Cerletti N., Bruggen J., Clerc R.G., Tarcsay L., Zwalbo G., Gerhards G., Schlegel R., Sorg C.;
"Two calcium-binding proteins in infiltrate macrophages of rheumatoid arthritis."; Nature 330:80-82(1987).
- [3] NUCLEOTIDE SEQUENCE [GENOMIC DNA].
PubMed=3405210
Lagasse E., Clerc R.G.;
"Cloning and expression of two human genes encoding calcium-binding proteins that are regulated during myeloid differentiation."; Mol. Cell. Biol. 8:2402-2410(1988).
- [4] NUCLEOTIDE SEQUENCE [mRNA], AND PROTEIN SEQUENCE OF 1-30.
PubMed=2039599
Schaefer T., Sachse G.E., Gassen H.G.;
"The calcium-binding protein MRP-8 is produced by human pulmonary tumor cells."; Biol. Chem. Hoppe-Seyler 372:1-4(1991).
- [5] NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].
Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
"Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)."; Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
- [6] NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].
Kalinine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y., Phelan M., Farmer A.;

"Cloning of human full-length CDSs in BD Creator(TM) system donor vector.";
 Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.

[7] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

DOI=10.1038/nature04727; PubMed=16710414

Gregory S.G., Barlow K.F., McLay K.E., Kaul R., Swarbreck D., Dunham A., Scott C.E., Howe K.L., Woodfine K., Spencer C.C.A., Jones M.C., Gillson C., Searle S., Zhou Y., Kokocinski F., McDonald L., Evans R., Phillips K., Atkinson A., Cooper R., Jones C., Hall R.E., Andrews T.D., Lloyd C., Ainscough R., Almeida J.P., Ambrose K.D., Anderson F., Andrew R.W., Ashwell R.I.S., Aubin K., Babbage A.K., Bagguley C.L., Bailey J., Beasley H., Bethel G., Bird C.P., Bray-Allen S., Brown J.Y., Brown A.J., Buckley D., Burton J., Bye J., Carder C., Chapman J.C., Clark S.Y., Clarke G., Clee C., Cobley V., Collier R.E., Corby N., Coville G.J., Davies J., Deadman R., Dunn M., Earthrow M., Ellington A.G., Errington H., Frankish A., Frankland J., French L., Garner P., Garnett J., Gay L., Ghori M.R.J., Gibson R., Gilby L.M., Gillett W., Glithero R.J., Grahams D.V., Griffiths C., Griffiths-Jones S., Grocock R., Hammond S., Harrison E.S.I., Hart E., Haugen E., Heath P.D., Holmes S., Holt K., Howden P.J., Hunt A.R., Hunt S.E., Hunter G., Isherwood J., James R., Johnson C., Johnson D., Joy A., Kay M., Kershaw J.K., Kubukawa M., Kimberley A.M., King A., Knights A.J., Lad H., Laird G., Lawlor S., Leongamornlert D.A., Lloyd D.M., Loveland J., Lovell J., Lush M.J., Lyne R., Martin S., Mashreghi-Mohammadi M., Matthews L., Matthews N.S.W., McLaren S., Milne S., Mistry S., Moore M.J.F., Nickerson T., O'Dell C.N., Oliver K., Palmeira A., Palmer S.A., Parker A., Patel D., Pearce A.V., Peck A.I., Pelan S., Phelps K., Phillimore B.J., Plumb R., Rajan J., Raymond C., Rouse G., Saenphimmachak C., Sehra H.K., Sheridan E., Shownkeen R., Sims S., Skuce C.D., Smith M., Steward C., Subramanian S., Sycamore N., Tracey A., Tromans A., Van Heimond Z., Wall M., Wallis J.M., White S., Whitehead S.L., Wilkinson J.E., Willey D.L., Williams H., Wilming L., Wray P.W., Wu Z., Coulson A., Vaudin M., Sulston J.E., Durbin R., Hubbard T., Wooster R., Dunham I., Carter N.P., McVean G., Ross M.T., Harrow J., Olson M.V., Beck S., Rogers J., Bentley D.R.;

"The DNA sequence and biological annotation of human chromosome 1.";
Nature 441:315-321(2006).

[8] NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].

TISSUE=Skeletal muscle;

DOI=10.1101/gr.2596504; PubMed=15489334

The MGC Project Team;

"The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC).";
Genome Res. 14:2121-2127(2004).

[9] PROTEIN SEQUENCE OF 1-19; 24-35 AND 63-89.

DOI=10.1006/bbrc.1996.0616; PubMed=8619876

Marti T., Ertmann K.D., Gallin M.Y.;

"Host-parasite interaction in human onchocerciasis: identification and sequence analysis of a novel human calgranulin.";
Biochem. Biophys. Res. Commun. 221:454-458(1996).

[10] PROTEIN SEQUENCE OF 1-27.

PubMed=8423249

Miyasaki K.T., Bodeau A.L., Murthy A.R., Lehrer R.I.;

"In vitro antimicrobial activity of the human neutrophil cytosolic S-100 protein complex, calprotectin, against Capnocytophaga sputigena.";

J. Dent. Res. 72:517-523(1993).

[11] PROTEIN SEQUENCE OF 1-20.

PubMed=7849642

Umekawa T., Kurita T.;

"Calprotectin-like protein is related to soluble organic matrix in calcium oxalate urinary stone.";

Biochem. Mol. Biol. Int. 34:309-313(1994).

[12] PROTEIN SEQUENCE OF 38-47 AND 50-56.

TISSUE=Keratinocyte;

PubMed=1286667

Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E., Vandekerckhove J.;

"Microsequences of 145 proteins recorded in the two-dimensional gel protein database of normal human epidermal keratinocytes.";

Electrophoresis 13:960-969(1992).

[13] X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

DOI=10.1107/S0907444900002833; PubMed=10771424

Ishikawa K., Nakagawa A., Tanaka I., Suzuki M., Nishihira J.;

"The structure of human MRP8, a member of the S100 calcium-binding protein family, by MAD phasing at 1.9 Å resolution.";

Acta Crystallogr. D 56:559-566(2000).

Comments

- **FUNCTION:** Expressed by macrophages in chronic inflammations. Also expressed in epithelial cells constitutively or induced during dermatoses. May interact with components of the intermediate filaments in monocytes and epithelial

cells.

- **SUBUNIT:** Homodimer.
- **MISCELLANEOUS:** Binds two calcium ions per molecule with an affinity similar to that of the S100 proteins.
- **SIMILARITY:** Belongs to the S-100 family.
- **SIMILARITY:** Contains 2 EF-hand domains.

Copyright

Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>. Distributed under the Creative Commons Attribution-NoDerivs License.

Cross-references

Sequence databases	
EMBL	Y00278; CAA68390.1; -; mRNA. X06234; CAA29580.1; -; mRNA. M21005; AAA36327.1; -; Genomic_DNA. CR407674; CAG28602.1; -; mRNA. BT007378; AAP36042.1; -; mRNA. AL591704; CAI19497.1; -; Genomic_DNA. BC005928; AAH05928.1; -; mRNA.
PIR	A31848; BCHUCF.
UniGene	Hs.416073
3D structure databases	
PDB	1MR8; X-ray; A/B=1-93. 1XK4; X-ray; A/B/E/F/I/J=1-93.
Protein-protein interaction databases	
DIP	DIP:1165N; -.
2D gel databases	
SWISS-2DPAGE	P05109; HUMAN.
Aarhus/Ghent-2DPAGE	1003; IEF.
PMMA-2DPAGE	P05109; -.
Organism-specific gene databases	
H-InvDB	HIX0001079; -.
HGNC	HGNC:10498; S100A8.
GeneCards	S100A8.
GeneLynx	S100A8; Homo sapiens.
GenAtlas	S100A8.
HPA	CAB002791; -.
MIM	123885; gene.
Gene expression databases	
CleanEx	HGNC:10498; S100A8.
ArrayExpress	P05109; -.
GermOnline	ENSG00000143546; Homo sapiens.
Ontologies	
GO	GO:0005509; Molecular function: calcium ion binding (<i>traceable author statement from ProtInc</i>). GO:0006954; Biological process: inflammatory response (<i>traceable author statement from ProtInc</i>).
Family and domain databases	
InterPro	IPR011992; EF-Hand_type. IPR002048; EF_hand_Ca_bd. IPR001751; S100_Ca_bd. IPR013787; S100_Ca_bd_sub.

Gene3D	G3DSA:1.10.238.10; EF-Hand_type; 1.
Pfam	PF00036; ehand; 1.
ProDom	PD003407; CaBP_S100; 1. PD000012; EF-hand; 1.
PROSITE	PS00018; EF_HAND_1; 1. PS0222; EF_HAND_2; 1. PS00303; S100_CABP; 1. PROSITE graphical view of domain structure (profiles).
Genome annotation databases	
Ensembl	ENSG00000143546; Homo sapiens.
KEGG	hsa:6279; --
Other	
RZPD-ProtExp	Clones: G0188, IOH7407, RZPDo834A1216, RZPDo839A1269
Implicit links to	SOURCE; HOVERGEN; BLOCKS; ProtoNet; ModBase; UniRef.

Keywords

3D-structure; Calcium; Direct protein sequencing; Repeat.

Features

Key	From	To	Length	Description	FTId
CHAIN	1	93	93	Protein S100-A8.	PRO_0000143993
DOMAIN	12	47	36	EF-hand 1.	
DOMAIN	46	81	36	EF-hand 2.	
CA_BIND	20	33	14	1; low affinity.	
CA_BIND	59	70	12	2; high affinity.	
CONFLICT	80	93		VAAHKKSHEESHKE -> WQPTKKAMKKATKSS (in Ref. 1; CAA68390).	
HELIX	4	20	17		
STRAND	22	25	4		
HELIX	31	41	11		
HELIX	44	47	4		
HELIX	51	58	8		
STRAND	63	66	4		
HELIX	68	86	19		

Sequence information

Length: 93 AA [This is the length of the unprocessed precursor]
Molecular weight: 10835 Da [This is the MW of the unprocessed precursor]
CRC64: 78F589140B9CE166 [This is a checksum on the sequence]

10	20	30	40	50	60
MLTELEKALN	SIIDVYHKYS	LIKGNFHAVY	RDDLKKLLET	ECPQYIRKKG	ADVWFKELDI
70	80	90			
NTDGAVNFQE	FLILVIKMGV	AAHKKSHHEES	HKE		

UniProtKB/Swiss-Prot entry P80511

Entry information

Entry name	S10AC_HUMAN
Primary accession number	P80511
Secondary accession numbers	P83219 Q5SY66
Integrated into Swiss-Prot on	October 1, 1996
Sequence was last modified on	January 23, 2007 (Sequence version 2)
Annotations were last modified on	March 20, 2007 (Entry version 70)

Name and origin of the protein

Protein name	Protein S100-A12
Synonyms	S100 calcium-binding protein A12 Calgranulin-C CAGC CGRP Neutrophil S100 protein Calcium-binding protein in amniotic fluid 1 CAAF1 p6
Contains	Calcitermin
Gene name	Name: S100A12
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

References

- [1] NUCLEOTIDE SEQUENCE [GENOMIC DNA / mRNA].
DOI=10.1016/S0143-4160(96)90087-1; PubMed=8985590
Wicki R., Marenholz I., Mischke D., Schaefer B.W., Heizmann C.W.;
"Characterization of the human S100A12 (calgranulin C, p6, CAAF1, CGRP) gene, a new member of the S100 gene cluster on chromosome 1q21.1";
Cell Calcium 20:459-464(1996).
- [2] NUCLEOTIDE SEQUENCE [GENOMIC DNA / mRNA].
DOI=10.1006/bbrc.1996.0600; PubMed=8619860
Yamamura T., Hitomi J., Nagasaki K., Suzuki M., Takahashi E., Saito S., Tsukada T., Yamaguchi K.;
"Human CAAF1 gene -- molecular cloning, gene structure, and chromosome mapping.";
Biochem. Biophys. Res. Commun. 221:356-360(1996).
- [3] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
DOI=10.1038/nature04727; PubMed=16710414
Gregory S.G., Barlow K.F., McLay K.E., Kaul R., Swarbreck D., Dunham A., Scott C.E., Howe K.L., Woodfine K., Spence C.C.A., Jones M.C., Gillson C., Searle S., Zhou Y., Kokocinski F., McDonald L., Evans R., Phillips K., Atkinson A., Cooper R., Jones C., Hall R.E., Andrews T.D., Lloyd C., Ainscough R., Almeida J.P., Ambrose K.D., Anderson F., Andrew R.W., Ashwell R.I.S., Aubin K., Babbage A.K., Bagguley C.L., Bailey J., Beasley H., Bethel G., Bird C.P., Bray-Allen S., Brown J.Y., Brown A.J., Buckley D., Burton J., Bye J., Carder C., Chapman J.C., Clark S.Y., Clarke G., Clee C., Cobley V., Collier R.E., Corby N., Coville G.J., Davies J., Deadman R., Dunn M., Earthrow M., Ellington A.G., Errington H., Frankish A., Frankland J., French L., Garner P., Garnett J., Gay L., Ghori M.R.J., Gibson R., Gilby L.M., Gillett W., Glithero R.J., Graham D.V., Griffiths C., Griffiths-Jones S., Grocock R., Hammond S., Harrison E.S.I., Hart E., Haugen E., Heath P.D., Holmes S., Holt K., Howden P.J., Hunt A.R., Hunt S.E., Hunter G., Isherwood J., James R., Johnson C., Johnson D., Joy A., Kay M., Kershaw J.K., Kubikawa M., Kimberley A.M., King A., Knights A.J., Lad H., Laird G., Lawlor S., Leongamornlert D.A., Lloyd D.M., Loveland J., Lovell J., Lush M.J., Lyne R., Martin S., Mashreghi-Mohammadi M., Matthews L., Matthew N.S.W., McLaren S., Milne S., Mistry S., Moore M.J.F., Nickerson T., O'Dell C.N., Oliver K., Palmeiri A., Palmer S.A., Parker A., Patel D., Pearce A.V., Peck A.I., Pelan S., Phelps K., Phillimore B.J., Plumb R., Rajan J., Raymond C., Rouse G., Saenphimmachak C., Sehra H.K., Sheridan E., Shownkeen R., Sims S., Skuce C.D., Smith M., Steward C., Subramanian S., Sycamore N., Tracey A., Tromans A., Van Helmond Z., Wall M., Wallis J.M., White S., Whitehead S.L., Wilkinson J.E., Willey D.L., Williams H., Wilming L., Wray P.W., Wu Z., Coulson A., Vaudin M., Sulston J.E., Durbin R., Hubbard T., Wooster R., Dunham I., Carter N.P., McVean G., Ross M.T., Harrow J., Olson M.V., Beck S., Rogers J.,

Bentley D.R.;
 "The DNA sequence and biological annotation of human chromosome 1.";
Nature 441:315-321(2006).

[4] NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].

TISSUE=Blood;
 DOI=10.1101/gr.2596504; PubMed=15489334
 The MGC Project Team;
 "The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC)." ;
Genome Res. 14:2121-2127(2004).

[5] PROTEIN SEQUENCE OF 2-92.

DOI=10.1006/bbrc.1996.0616; PubMed=8619876
 Marti T., Ertmann K.D., Gallin M.Y.;
 "Host-parasite interaction in human onchocerciasis: identification and sequence analysis of a novel human calgranulin." ;
Biochem. Biophys. Res. Commun. 221:454-458(1996).

[6] PROTEIN SEQUENCE OF 2-92.

TISSUE=Neutrophil;
 DOI=10.1006/bbrc.1996.1144; PubMed=8769108
 Ilg E.C., Troxler H., Buergisser D.M., Kuster T., Markert M., Guignard F., Hunziker P., Birchler N., Heizmann C.W.;
 "Amino acid sequence determination of human S100A12 (P6, calgranulin C, CGRP, CAAF1) by tandem mass spectrometry." ;
Biochem. Biophys. Res. Commun. 225:146-150(1996).

[7] PROTEIN SEQUENCE OF 2-21.

PubMed=7626002
 Guignard F., Mauel J., Markert M.;
 "Identification and characterization of a novel human neutrophil protein related to the S100 family." ;
Biochem. J. 309:395-401(1995).

[8] PROTEIN SEQUENCE OF 78-92, ANTIMICROBIAL ACTIVITY, AND MASS SPECTROMETRY.

TISSUE=Nasal mucus;
 DOI=10.1016/S0014-5793(01)02731-4; PubMed=11522286
 Cole A.M., Kim Y.-H., Tahk S., Hong T., Weis P., Waring A.J., Ganz T.;
 "Calcitermin, a novel antimicrobial peptide isolated from human airway secretions." ;
FEBS Lett. 504:5-10(2001).

[9] X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).

DOI=10.1107/S090744490001458X; PubMed=11134923
 Moroz O.V., Antson A.A., Murshudov G.N., Maitland N.J., Dodson G.G., Wilson K.S., Skibshoj I., Lukyanidin E.M.,
 Bronstein I.B.;
 "The three-dimensional structure of human S100A12." ;
Acta Crystallogr. D 57:20-29(2001).

Comments

- **FUNCTION:** Calcitermin possesses antifungal activity against *C.albicans* and is also active against *E.coli* and *P.aeruginosa* but not *L.monocytogenes* and *S.aureus*.
- **SUBUNIT:** Homodimer.
- **TISSUE SPECIFICITY:** Monocytes and lymphocytes.
- **MASS SPECTROMETRY:** MW=10444; METHOD=Electrospray; RANGE=2-92; NOTE=Ref.8.
- **MASS SPECTROMETRY:** MW=1688.9; METHOD=MALDI; RANGE=78-92; NOTE=Ref.8.
- **SIMILARITY:** Belongs to the S-101 family.
- **SIMILARITY:** Contains 2 EF-hand domains.

Copyright

Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>. Distributed under the Creative Commons Attribution-NoDerivs License.

Cross-references

Sequence databases

X97859; CAA66453.1; -; mRNA. X98288; CAA66934.1; -; Genomic_DNA. X98289; CAA66934.1; JOINED; Genomic_DNA. X98290; CAA66934.1; JOINED; Genomic_DNA. X98289; CAB94792.1; -; Genomic_DNA.
--

EMBL	X98290; CAB94792.1; JOINED; Genomic_DNA. D49549; BAA08497.1; -; mRNA. D83664; BAA12036.1; -; mRNA. D83657; BAA12030.1; -; Genomic_DNA. AL591704; CAI19495.1; -; Genomic_DNA. BC070294; AAH70294.1; -; mRNA.
	PIR JC4712; JC4712.
	UniGene Hs.19413
	3D structure databases
	PDB 1E8A; X-ray; A/B=1-92. 1GQM; X-ray; A/B/C/D/E/F/G/H/I/J/K/L=1-92. 1ODB; X-ray; A/B/C/D/E/F=1-92.
Organism-specific gene databases	
HGNC	HGNC:10489; S100A12.
GeneCards	S100A12.
GeneLynx	S100A12; Homo sapiens.
GenAtlas	S100A12.
MIM	603112; gene.
Gene expression databases	
CleanEx	HGNC:10489; S100A12.
ArrayExpress	P80511; -.
GermOnline	ENSG00000163221; Homo sapiens.
Ontologies	
GO	GO:0005829; Cellular component: cytosol (<i>traceable author statement from ProtInc</i>). GO:0005626; Cellular component: insoluble fraction (<i>traceable author statement from ProtInc</i>). GO:0005509; Molecular function: calcium ion binding (<i>traceable author statement from ProtInc</i>). GO:0008270; Molecular function: zinc ion binding (<i>traceable author statement from UniProtKB</i>). GO:0050832; Biological process: defense response to fungus (<i>inferred from direct assay from UniProtKB</i>). GO:0006954; Biological process: inflammatory response (<i>traceable author statement from ProtInc</i>). GO:0006805; Biological process: xenobiotic metabolic process (<i>inferred from direct assay from UniProtKB</i>).
Family and domain databases	
InterPro	IPR011992; EF-Hand_type. IPR002048; EF_hand_Ca_bd. IPR001751; S100_Ca_bd. IPR013787; S100_Ca_bd_sub.
Gene3D	G3DSA:1.10.238.10; EF-Hand_type; 1.
Pfam	PF00036; ehand; 1.
ProDom	PD003407; CaBP_S100; 1. PD000012; EF-hand; 1.
PROSITE	PS00018; EF_HAND_1; FALSE_NEG. PS50222; EF_HAND_2; 1. PS00303; S100_CABP; 1. PROSITE graphical view of domain structure (profiles).
Genome annotation databases	
Ensembl	ENSG00000163221; Homo sapiens.
KEGG	hsa:6283; -.
Other	
RZPD-ProtExp	Clones: I0294, IOH40815
Implicit links to	SOURCE; HOVERGEN; BLOCKS; ProtoNet; ModBase; UniRef.

Keywords

3D-structure; Antibiotic; Antimicrobial; Calcium; Direct protein sequencing; Fungicide; Metal-binding; Repeat; Zinc.

Features

Key	From	To	Length	Description	FTId
INIT_MET	1	1	1	Removed.	
CHAIN	2	92	91	Protein S100-A12.	PRO_0000045383
PEPTIDE	78	92	15	Calcitermin.	PRO_000004774
DOMAIN	13	48	36	EF-hand 1.	
DOMAIN	49	84	36	EF-hand 2.	
CA_BIND	19	32	14	1; low affinity (By similarity).	
CA_BIND	62	73	12	2; high affinity (By similarity).	
HELIX	2	18	17		
STRAND	20	22	3		
HELIX	29	39	11		
TURN	41	43	3		
TURN	45	48	4		
HELIX	50	60	11		
HELIX	70	89	20		

Sequence information

Length: 92 AA [This is the length of the unprocessed precursor]
Molecular weight: 10575 Da [This is the MW of the unprocessed precursor]
CRC64: 52AF75A31BDC222A [This is a checksum on the sequence]

10 20 30 40 50 60
MTKLEEHLEG IVNIFHQYSV RKGHFDTLSK GELKQLLTKE LANTIKNIKD KAVIDEIFQG
70 80 90
LDANQDEQVD FQEFLISLVAI ALKAAHYHTH KE

EBI Uniprot UniSave

The UniProtKB Sequence/Annotation Version Archive (UniSave) is a repository of UniProtKB/Swiss-Prot and UniProtKB/TrEMBL versions.

Primary accession number or entry name:

Date: day-month-year (e.g. 30-11-1998 or 30-NOV-1998) or year-month-day.

[<< Earlier](#) [Later >>](#)

P80511 12-DEC-2006

[<< Earlier](#) [Later >>](#)

P80511 23-JAN-2007

[Back to List](#)

ID S10AC_HUMAN Reviewed; 92 AA.
ID S10AC_HUMAN Reviewed; 91 AA.
AC P80511; P83219;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 23-JAN-2007, sequence version 2.
DT 23-JAN-2007, entry version 67.
DT 01-OCT-1996, sequence version 1.
DT 12-DEC-2006, entry version 66.
DE Protein S100-A12 (S100 calcium-binding protein A12) (Calgranulin-C)
DE (CAGC) (CGRP) (Neutrophil S100 protein) (Calcium-binding protein in
DE amniotic fluid 1) (CAAF1) (p6) [Contains: Calcitermin].
GN Name=S100A12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / mRNA].
RX MEDLINE=97138564; PubMed=8985590; DOI=10.1016/S0143-4160(96)90087-1;
RA Wicki R., Marenholz I., Mischke D., Schaefer B.W., Heizmann C.W.;
RT "Characterization of the human S100A12 (calgranulin C, p6, CAAF1,
RT CGRP) gene, a new member of the S100 gene cluster on chromosome
RT 1q21.";
RL Cell Calcium 20:459-464(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / mRNA].
RX MEDLINE=96192053; PubMed=8619860; DOI=10.1006/bbrc.1996.0600;
RA Yamamura T., Hitomi J., Nagasaki K., Suzuki M., Takahashi E.,
RA Saito S., Tsukada T., Yamaguchi K.;
RT "Human CAAF1 gene -- molecular cloning, gene structure, and chromosome
RT mapping.";
RL Biochem. Biophys. Res. Commun. 221:356-360(1996).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].
RC TISSUE=Blood;
RX PubMed=15489334; DOI=10.1101/gr.2596504;
RG The MGC Project Team;
RT "The status, quality, and expansion of the NIH full-length cDNA
RT project: the Mammalian Gene Collection (MGC)." ;
RL Genome Res. 14:2121-2127(2004).
RN [4]
RP PROTEIN SEQUENCE OF 2-92.
RP PROTEIN SEQUENCE.
RX MEDLINE=96192069; PubMed=8619876; DOI=10.1006/bbrc.1996.0616;
RA Marti T., Ertmann K.D., Gallin M.Y.;
RT "Host-parasite interaction in human onchocerciasis: identification and
RT sequence analysis of a novel human calgranulin.";
RL Biochem. Biophys. Res. Commun. 221:454-458(1996).
DN 151

RP PROTEIN SEQUENCE OF 2-92.
RN [4]
RP PROTEIN SEQUENCE.
RC TISSUE=Neutrophil;
RX MEDLINE=96332419; PubMed=8769108; DOI=10.1006/bbrc.1996.1144;
RA Ilg E.C., Troxler H., Buergisser D.M., Kuster T., Markert M.,
RA Guignard F., Hunziker P., Birchler N., Heizmann C.W.;
RT "Amino acid sequence determination of human S100A12 (P6, calgranulin
RT C, CGRP, CAAF1) by tandem mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 225:146-150(1996).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].
RC TISSUE=Blood;
RX PubMed=15489334; DOI=10.1101/gr.2596504;
RG The MGC Project Team;
RT "The status, quality, and expansion of the NIH full-length cDNA
RT project: the Mammalian Gene Collection (MGC).";
RL Genome Res. 14:2121-2127(2004).
RN [6]
RP PROTEIN SEQUENCE OF 2-21.
RP PROTEIN SEQUENCE OF 1-20.
RX MEDLINE=95351965; PubMed=7626002;
RA Guignard F., Mael J., Markert M.;
RT "Identification and characterization of a novel human neutrophil
RT protein related to the S100 family.";
RL Biochem. J. 309:395-401(1995).
RN [7]
RP PROTEIN SEQUENCE OF 78-92, ANTIMICROBIAL ACTIVITY, AND MASS
RP PROTEIN SEQUENCE OF 77-91, ANTIMICROBIAL ACTIVITY, AND MASS
RP SPECTROMETRY.
RC TISSUE=Nasal mucus;
RX MEDLINE=21413725; PubMed=11522286; DOI=10.1016/S0014-5793(01)02731-4;
RA Cole A.M., Kim Y.-H., Tahk S., Hong T., Weis P., Waring A.J., Ganz T.;
RT "Calcitermin, a novel antimicrobial peptide isolated from human airway
RT secretions.";
RL FEBS Lett. 504:5-10(2001).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
RX MEDLINE=21065388; PubMed=11134923; DOI=10.1107/S090744490001458X;
RA Moroz O.V., Antson A.A., Murshudov G.N., Maitland N.J., Dodson G.G.,
RA Wilson K.S., Skibshoj I., Lukanidin E.M., Bronstein I.B.;
RT "The three-dimensional structure of human S100A12.";
RL Acta Crystallogr. D 57:20-29(2001).
CC --!- FUNCTION: Calcitermin possesses antifungal activity against
CC C.albicans and is also active against E.coli and P.aeruginosa but
CC not L.monocytogenes and S.aureus.
CC --!- SUBUNIT: Homodimer.
CC --!- TISSUE SPECIFICITY: Monocytes and lymphocytes.
CC --!- MASS SPECTROMETRY: MW=10444; METHOD=Electrospray; RANGE=2-92;
CC --!- MASS SPECTROMETRY: MW=10444; METHOD=Electrospray; RANGE=1-91;
CC NOTE=Ref.7.
CC --!- MASS SPECTROMETRY: MW=1688.9; METHOD=MALDI; RANGE=78-92;
CC --!- MASS SPECTROMETRY: MW=1688.9; METHOD=MALDI; RANGE=77-91;
CC NOTE=Ref.7.
CC --!- SIMILARITY: Belongs to the S-101 family.
CC --!- SIMILARITY: Belongs to the S-100 family.
CC --!- SIMILARITY: Contains 2 EF-hand domains.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; X97859; CAA66453.1; -; mRNA.
DR EMBL; X98288; CAA66934.1; -; Genomic_DNA.
DR EMBL; X98289; CAA66934.1; JOINED; Genomic_DNA.
DR EMBL; X98290; CAA66934.1; JOINED; Genomic_DNA.

DR EMBL; X98289; CAB94792.1; -; Genomic_DNA.
DR EMBL; X98290; CAB94792.1; JOINED; Genomic_DNA.
DR EMBL; D49549; BAA08497.1; -; mRNA.
DR EMBL; D83664; BAA12036.1; -; mRNA.
DR EMBL; D83657; BAA12030.1; -; Genomic_DNA.
DR EMBL; BC070294; AAH70294.1; -; mRNA.
DR PIR; JC4712; JC4712.
DR UniGene; Hs.19413; -.
DR PDB; 1E8A; X-ray; A/B=1-92.
DR PDB; 1GQM; X-ray; A/B/C/D/E/F/G/H/I/J/K/L=1-92.
DR PDB; 1ODB; X-ray; A/B/C/D/E/F=1-92.
DR PDB; 1E8A; X-ray; A/B=1-91.
DR PDB; 1GQM; X-ray; A/B/C/D/E/F/G/H/I/J/K/L=1-91.
DR PDB; 1ODB; X-ray; A/B/C/D/E/F=1-91.
DR GermOnline; ENSG00000163221; Homo sapiens.
DR Ensembl; ENSG00000163221; Homo sapiens.
DR KEGG; hsa:6283; -.
DR HGNC; HGNC:10489; S100A12.
DR MIM; 603112; gene.
DR ArrayExpress; P80511; -.
DR GermOnline; ENSG00000163221; Homo sapiens.
DR RZPD-ProtExp; I0294; -.
DR RZPD-ProtExp; IOH40815; -.
DR GO; GO:0005829; C:cytosol; TAS:ProtInc.
DR GO; GO:0005626; C:insoluble fraction; TAS:ProtInc.
DR GO; GO:0005509; F:calcium ion binding; TAS:ProtInc.
DR GO; GO:0008270; F:zinc ion binding; TAS:UniProtKB.
DR GO; GO:0050832; P:defense response to fungus; IDA:UniProtKB.
DR GO; GO:0006954; P:inflammatory response; TAS:ProtInc.
DR GO; GO:0006805; P:xenobiotic metabolism; IDA:UniProtKB.
DR InterPro; IPR011992; EF-Hand_type.
DR InterPro; IPR002048; EF_hand_Ca_bd.
DR InterPro; IPR001751; S100_Ca_bd.
DR InterPro; IPR013787; S100_Ca_bd_sub.
DR Gene3D; G3DSA:1.10.238.10; EF-Hand_type; 1.
DR Pfam; PF00036; eftand; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF_HAND_1; FALSE_NEG.
DR PROSITE; PS50222; EF_HAND_2; 1.
DR PROSITE; PS00303; S100_CABP; 1.
KW 3D-structure; Antibiotic; Antimicrobial; Calcium;
KW Direct protein sequencing; Fungicide; Metal-binding; Repeat; Zinc.
FT INIT_MET 1 1 Removed.
FT CHAIN 2 92 Protein S100-A12.
FT INIT_MET 0 0
FT CHAIN 1 91 Protein S100-A12.
FT /FTId=PRO_0000045383.
FT PEPTIDE 78 92 Calcitermin.
FT PEPTIDE 77 91 Calcitermin.
FT /FTId=PRO_0000004774.
FT DOMAIN 13 48 EF-hand 1.
FT DOMAIN 49 84 EF-hand 2.
FT CA_BIND 19 32 1; low affinity (By similarity).
FT CA_BIND 62 73 2; high affinity (By similarity).
FT HELIX 3 19
FT TURN 20 20
FT STRAND 21 24
FT TURN 25 26
FT HELIX 30 40
FT TURN 42 44
FT TURN 46 49
FT HELIX 51 61
FT TURN 63 64
FT HELIX 71 87
SQ SEQUENCE 92 AA; 10575 MW; 52AF75A31BDC222A CRC64;

MTKLEEHLEG IVNIFHQYSV RKGHFDTLSK GELKQLLTKE LANTIKNIKD KAVIDEIFQG

LDANQDEQVD FQEFISLVAI ALKAAYHHTH KE
FT DOMAIN 12 47 EF-hand 1.
FT DOMAIN 48 83 EF-hand 2.
FT CA_BIND 18 31 1; low affinity (By similarity).
FT CA_BIND 61 72 2; high affinity (By similarity).
FT HELIX 2 18
FT TURN 19 19
FT STRAND 20 23
FT TURN 24 25
FT HELIX 29 39
FT TURN 41 43
FT TURN 45 48
FT HELIX 50 60
FT TURN 62 63
FT HELIX 70 86
SQ SEQUENCE 91 AA; 10444 MW; 325685EA8695F6B7 CRC64;
TKLEEHLEGI VNIFHQYSVR KGHFDTLSKG ELKQLLTKE ANTIKNIKDK AVIDEIFQGL
DANQDEQVDF QEFISLVAIA LKAAYHHTHK E
//

100.000% identity (Smith-Waterman score: 577)

[Show Help](#)